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#2

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/944,849

DATE: 09/21/2001
TIME: 18:10:39

Input Set : A:\ES.txt
Output Set: N:\CRF3\09212001\I944849.raw

3 <110> APPLICANT: Nickoloff, Brian
4 Miele, Lucio
6 <120> TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND
TREATMENT OF
7 MALIGNANT AND BENIGN SKIN DISORDERS BY MODULATING THE NOTCH PATHWAY
9 <130> FILE REFERENCE: 212583
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/944,849
12 <141> CURRENT FILING DATE: 2001-08-31
14 <150> PRIOR APPLICATION NUMBER: US 60/229,614
15 <151> PRIOR FILING DATE: 2000-08-31
17 <160> NUMBER OF SEQ ID NOS: 18
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 7332
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial Sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Constitutively Active Notch-1
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(7332)
32 <223> OTHER INFORMATION:
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (5288)..(5288)
38 <223> OTHER INFORMATION: n is "a," "t," "g," or "c"
41 <220> FEATURE:
42 <221> NAME/KEY: misc_feature
43 <222> LOCATION: (5359)..(5359)
44 <223> OTHER INFORMATION: n is "a," "t," "g," or "c"
47 <400> SEQUENCE: 1
48 atg ccg ccg ctc ctg gcg ccc ctg ctc tgc ctg gcg ctg ctg ccc gcg 48
49 Met Pro Pro Leu Leu Ala Pro Leu Leu Cys Leu Ala Leu Leu Pro Ala
50 1 5 10 15
52 ctc gcc gca cga ggc ccg cga tgc tcc cag ccc ggt gag acc tgc ctg 96
53 Leu Ala Ala Arg Gly Pro Arg Cys Ser Gln Pro Gly Glu Thr Cys Leu
54 20 25 30
56 aat ggc ggg aag tgt gaa gcg gcc aat ggc acg gag gcc tgc gtc tgt 144
57 Asn Gly Gly Lys Cys Glu Ala Ala Asn Gly Thr Glu Ala Cys Val Cys
58 35 40 45
60 ggc ggg gcc ttc gtg ggc ccg cga tgc cag gac ccc aac ccg tgc ctc 192
61 Gly Gly Ala Phe Val Gly Pro Arg Cys Gln Asp Pro Asn Pro Cys Leu
62 50 55 60
64 agc acc ccc tgc aag aac gcg ggg aca tgc cac gtg gtg gac cgc aga 240
65 Ser Thr Pro Cys Lys Asn Ala Gly Thr Cys His Val Val Asp Arg Arg
66 65 70 75 80
68 ggc gtg gca gac tat gcc tgc agc tgt gcc ctg ggc ttc tct ggg ccc 288
69 Gly Val Ala Asp Tyr Ala Cys Ser Cys Ala Leu Gly Phe Ser Gly Pro

P.5
ENTERED

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70	85	90	95	
72	ctc tgc ctg aca ccc ctg gac aac gcc tgc ctc acc aac ccc tgc cgc			336
73	Leu Cys Leu Thr Pro Leu Asp Asn Ala Cys Leu Thr Asn Pro Cys Arg			
74	100	105	110	
76	aac ggg ggc acc tgc gac ctg ctc acg ctg acg gag tac aag tgc cgc			384
77	Asn Gly Gly Thr Cys Asp Leu Leu Thr Leu Thr Glu Tyr Lys Cys Arg			
78	115	120	125	
80	tgc ccc ccc ggc tgg tca ggg aaa tcg tgc cag cag gct gac ccg tgc			432
81	Cys Pro Pro Gly Trp Ser Gly Lys Ser Cys Gln Gln Ala Asp Pro Cys			
82	130	135	140	
84	gcc tcc aac ccc tgc gcc aac ggt ggc cag tgc ctg ccc ttc gag gcc			480
85	Ala Ser Asn Pro Cys Ala Asn Gly Gly Gln Cys Leu Pro Phe Glu Ala			
86	145	150	155	160
88	tcc tac atc tgc cac tgc cca ccc agc ttc cat ggc ccc acc tgc cgg			528
89	Ser Tyr Ile Cys His Cys Pro Pro Ser Phe His Gly Pro Thr Cys Arg			
90	165	170	175	
92	cag gat gtc aac gag tgt ggc cag aag ccc agg ctt tgc cgc cac gga			576
93	Gln Asp Val Asn Glu Cys Gly Gln Lys Pro Arg Leu Cys Arg His Gly			
94	180	185	190	
96	ggc acc tgc cac aac gag gtc ggc tcc tac cgc tgc gtc tgc cgc gcc			624
97	Gly Thr Cys His Asn Glu Val Gly Ser Tyr Arg Cys Val Cys Arg Ala			
98	195	200	205	
100	acc cac act ggc ccc aac tgc gag cgg ccc tac gtg ccc tgc agc ccc			672
101	Thr His Thr Gly Pro Asn Cys Glu Arg Pro Tyr Val Pro Cys Ser Pro			
102	210	215	220	
104	tcg ccc tgc cag aac ggg ggc acc tgc cgc ccc acg ggc gac gtc acc			720
105	Ser Pro Cys Gln Asn Gly Gly Thr Cys Arg Pro Thr Gly Asp Val Thr			
106	225	230	235	240
108	cac gag tgt gcc tgc ctg cca ggc ttc acc ggc cag aac tgt gag gaa			768
109	His Glu Cys Ala Cys Leu Pro Gly Phe Thr Gly Gln Asn Cys Glu Glu			
110	245	250	255	
112	aat atc gac gat tgt cca gga aac aac tgc aag aac ggg ggt gcc tgt			816
113	Asn Ile Asp Asp Cys Pro Gly Asn Asn Cys Lys Asn Gly Gly Ala Cys			
114	260	265	270	
116	gtg gac ggc gtg aac acc tac aac tgc ccg tgc ccg cca gag tgg aca			864
117	Val Asp Gly Val Asn Thr Tyr Asn Cys Pro Cys Pro Pro Glu Trp Thr			
118	275	280	285	
120	ggt cag tac tgt acc gag gat gtg gac gag tgc cag ctg atg cca aat			912
121	Gly Gln Tyr Cys Thr Glu Asp Val Asp Glu Cys Gln Leu Met Pro Asn			
122	290	295	300	
124	gcc tgc cag aac ggc ggg acc tgc cac aac acc cac ggt ggc tac aac			960
125	Ala Cys Gln Asn Gly Gly Thr Cys His Asn Thr His Gly Gly Tyr Asn			
126	305	310	315	320
128	tgc gtg tgt gtc aac ggc tgg act ggt gag gac tgc agc gag aac att			1008
129	Cys Val Cys Val Asn Gly Trp Thr Gly Glu Asp Cys Ser Glu Asn Ile			
130	325	330	335	
132	gat gac tgt gcc agc gcc gcc tgc ttc cac ggc gcc acc tgc cat gac			1056
133	Asp Asp Cys Ala Ser Ala Cys Phe His Gly Ala Thr Cys His Asp			
134	340	345	350	

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136	cgt	gtg	gcc	tcc	ttt	tac	tgc	gag	tgt	ccc	cat	ggc	cgc	aca	ggt	ctg	1104
137	Arg	Val	Ala	Ser	Phe	Tyr	Cys	Glu	Cys	Pro	His	Gly	Arg	Thr	Gly	Leu	
138	355															365	
140	ctg	tgc	cac	ctc	aac	gac	gca	tgc	atc	agc	aac	ccc	tgt	aac	gag	ggc	1152
141	Leu	Cys	His	Leu	Asn	Asp	Ala	Cys	Ile	Ser	Asn	Pro	Cys	Asn	Glu	Gly	
142	370															380	
144	tcc	aac	tgc	gac	acc	aac	cct	gtc	aat	ggc	aag	gcc	atc	tgc	acc	tgc	1200
145	Ser	Asn	Cys	Asp	Thr	Asn	Pro	Val	Asn	Gly	Lys	Ala	Ile	Cys	Thr	Cys	
146	385															400	
148	ccc	tcg	ggg	tac	acg	ggc	ccg	gcc	tgc	agc	cag	gac	gtg	gat	gag	tgc	1248
149	Pro	Ser	Gly	Tyr	Thr	Gly	Pro	Ala	Cys	Ser	Gln	Asp	Val	Asp	Glu	Cys	
150	405															415	
152	tcg	ctg	ggt	gcc	aac	ccc	tgc	gag	cat	gcg	ggc	aag	tgc	atc	aac	acg	1296
153	Ser	Leu	Gly	Ala	Asn	Pro	Cys	Glu	His	Ala	Gly	Lys	Cys	Ile	Asn	Thr	
154	420															430	
156	ctg	ggc	tcc	tcc	gag	tgc	cag	tgt	ctg	cag	ggc	tac	acg	ggc	ccc	cga	1344
157	Leu	Gly	Ser	Phe	Glu	Cys	Gln	Cys	Leu	Gln	Gly	Tyr	Thr	Gly	Pro	Arg	
158	435															445	
160	tgc	gag	atc	gac	gtc	aac	gag	tgc	gtc	tcg	aac	ccg	tgc	cag	aac	gac	1392
161	Cys	Glu	Ile	Asp	Val	Asn	Glu	Cys	Val	Ser	Asn	Pro	Cys	Gln	Asn	Asp	
162	450															460	
164	gcc	acc	tgc	ctg	gac	cag	att	ggg	gag	ttc	cag	tgc	atg	tgc	atg	ccc	1440
165	Ala	Thr	Cys	Leu	Asp	Gln	Ile	Gly	Glu	Phe	Gln	Cys	Met	Cys	Met	Pro	
166	465															480	
168	ggc	tac	gag	ggt	gtg	cac	tgc	gag	gtc	aac	aca	gac	gag	tgt	gcc	acg	1488
169	Gly	Tyr	Glu	Gly	Val	His	Cys	Glu	Val	Asn	Thr	Asp	Glu	Cys	Ala	Ser	
170	485															495	
172	agc	ccc	tgc	ctg	cac	aat	ggc	cgc	tgc	ctg	gac	aag	atc	aat	gag	ttc	1536
173	Ser	Pro	Cys	Leu	His	Asn	Gly	Arg	Cys	Leu	Asp	Lys	Ile	Asn	Glu	Phe	
174	500															510	
176	cag	tgc	gag	tgc	ccc	acg	ggc	ttc	act	ggg	cat	ctg	tgc	cag	tac	gat	1584
177	Gln	Cys	Glu	Cys	Pro	Thr	Gly	Phe	Thr	Gly	His	Leu	Cys	Gln	Tyr	Asp	
178	515															525	
180	gtg	gac	gag	tgt	gcc	agc	acc	ccc	tgc	aag	aat	ggt	gcc	aag	tgc	ctg	1632
181	Val	Asp	Glu	Cys	Ala	Ser	Thr	Pro	Cys	Lys	Asn	Gly	Ala	Lys	Cys	Leu	
182	530															540	
184	gac	gga	ccc	aac	act	tac	acc	tgt	gtg	tgc	acg	gaa	ggg	tac	acg	ggg	1680
185	Asp	Gly	Pro	Asn	Thr	Tyr	Thr	Cys	Val	Cys	Thr	Glu	Gly	Tyr	Thr	Gly	
186	545															560	
188	acg	cac	tgc	gag	gtg	gac	atc	gat	gag	tgc	gac	ccc	gac	ccc	tgc	cac	1728
189	Thr	His	Cys	Glu	Val	Asp	Ile	Asp	Glu	Cys	Asp	Pro	Asp	Pro	Cys	His	
190	565															575	
192	tac	ggc	tcc	tgc	aag	gac	ggc	gtc	gcc	acc	ttc	acc	tgc	ctc	tgc	cgc	1776
193	Tyr	Gly	Ser	Cys	Lys	Asp	Gly	Val	Ala	Thr	Phe	Thr	Cys	Leu	Cys	Arg	
194	580															590	
196	cca	ggc	tac	acg	ggc	cac	cac	tgc	gag	acc	aac	atc	aac	gag	tgc	tcc	1824
197	Pro	Gly	Tyr	Thr	Gly	His	His	Cys	Glu	Thr	Asn	Ile	Asn	Glu	Cys	Ser	
198	595															605	
200	agc	cag	ccc	tgc	cgc	cta	cgg	ggc	acc	tgc	cag	gac	ccg	gac	aac	gcc	1872

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201	Ser	Gln	Pro	Cys	Arg	Leu	Arg	Gly	Thr	Cys	Gln	Asp	Pro	Asp	Asn	Ala	
202	610					615					620						
204	tac	ctc	tgc	ttc	tgc	ctg	aag	ggg	acc	aca	gga	ccc	aac	tgc	gag	atc	1920
205	Tyr	Leu	Cys	Phe	Cys	Leu	Lys	Gly	Thr	Thr	Gly	Pro	Asn	Cys	Glu	Ile	
206	625					630					635					640	
208	aac	ctg	gat	gac	tgt	gcc	agc	agc	ccc	tgc	gac	tcg	ggc	acc	tgt	ctg	1968
209	Asn	Leu	Asp	Asp	Cys	Ala	Ser	Ser	Pro	Cys	Asp	Ser	Gly	Thr	Cys	Leu	
210						645					650					655	
212	gac	aag	atc	gat	ggc	tac	gag	tgt	gcc	tgt	gag	ccg	ggc	tac	aca	ggg	2016
213	Asp	Lys	Ile	Asp	Gly	Tyr	Glu	Cys	Ala	Cys	Glu	Pro	Gly	Tyr	Thr	Gly	
214						660					665					670	
216	agc	atg	tgt	aac	agc	aac	atc	gat	gag	tgt	gct	ggc	aac	ccc	tgc	cac	2064
217	Ser	Met	Cys	Asn	Ser	Asn	Ile	Asp	Glu	Cys	Ala	Gly	Asn	Pro	Cys	His	
218						675					680					685	
220	aac	ggg	ggc	acc	tgc	gag	gac	ggc	atc	aat	ggc	ttc	acc	tgc	cgc	tgc	2112
221	Asn	Gly	Gly	Thr	Cys	Glu	Asp	Gly	Ile	Asn	Gly	Phe	Thr	Cys	Arg	Cys	
222						690					695					700	
224	ccc	gag	ggc	tac	cac	gac	ccc	acc	tgc	ctg	tct	gag	gtc	aat	gag	tgc	2160
225	Pro	Glu	Gly	Tyr	His	Asp	Pro	Thr	Cys	Leu	Ser	Glu	Val	Asn	Glu	Cys	
226						705					710					715	
228	aac	agc	aac	ccc	tgc	cac	ggg	gcc	tgc	cg	gac	agc	ctc	aac	ggg		2208
229	Asn	Ser	Asn	Pro	Cys	Val	His	Gly	Ala	Cys	Arg	Asp	Ser	Leu	Asn	Gly	
230						725					730					735	
232	tac	aag	tgc	gac	tgt	gac	cct	ggg	tgg	agt	ggg	acc	aac	tgt	gac	atc	2256
233	Tyr	Lys	Cys	Asp	Cys	Asp	Pro	Gly	Trp	Ser	Gly	Thr	Asn	Cys	Asp	Ile	
234						740					745					750	
236	aac	aac	aac	gag	tgt	gaa	tcc	aac	cct	tgt	gtc	aac	ggc	ggc	acc	tgc	2304
237	Asn	Asn	Asn	Glu	Cys	Glu	Ser	Asn	Pro	Cys	Val	Asn	Gly	Gly	Thr	Cys	
238						755					760					765	
240	aaa	gac	atg	acc	agt	ggc	atc	gtg	tgc	acc	tgc	cg	gag	ggc	ttc	agc	2352
241	Lys	Asp	Met	Thr	Ser	Gly	Ile	Val	Cys	Thr	Cys	Arg	Glu	Gly	Phe	Ser	
242						770					775					780	
244	ggt	ccc	aac	tgc	cag	acc	aac	atc	aac	gag	tgt	gtc	tcc	aac	cca	tgt	2400
245	Gly	Pro	Asn	Cys	Gln	Thr	Asn	Ile	Asn	Glu	Cys	Ala	Ser	Asn	Pro	Cys	
246						785					790					795	
248	ctg	aac	aag	ggc	acg	tgt	att	gac	gac	gtt	gcc	ggg	tac	aag	tgc	aac	2448
249	Leu	Asn	Lys	Gly	Thr	Cys	Ile	Asp	Asp	Val	Ala	Gly	Tyr	Lys	Cys	Asn	
250						805					810					815	
252	tgc	ctg	ccc	tac	aca	ggt	gcc	acg	tgt	gag	gtg	gtg	ctg	gcc	ccg		2496
253	Cys	Leu	Leu	Pro	Tyr	Thr	Gly	Ala	Thr	Cys	Glu	Val	Val	Leu	Ala	Pro	
254						820					825					830	
256	tgt	gcc	ccc	agc	ccc	tgc	aga	aac	ggc	ggg	gag	tgc	agg	caa	tcc	gag	2544
257	Cys	Ala	Pro	Ser	Pro	Cys	Arg	Asn	Gly	Gly	Glu	Cys	Arg	Gln	Ser	Glu	
258						835					840					845	
260	gac	tat	gag	agc	ttc	tcc	tgt	gtc	ccc	acg	gct	ggg	gcc	aaa	ggg		2592
261	Asp	Tyr	Glu	Ser	Phe	Ser	Cys	Val	Cys	Pro	Thr	Ala	Gly	Ala	Lys	Gly	
262						850					855					860	
264	cag	acc	tgt	gag	gtc	gac	atc	aac	gag	tgc	gtt	ctg	agc	ccg	tgc	cg	2640
265	Gln	Thr	Cys	Glu	Val	Asp	Ile	Asn	Glu	Cys	Val	Leu	Ser	Pro	Cys	Arg	

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266	865	870	875	880														
268	cac	ggc	gca	tcc	tgc	cag	aac	acc	cac	ggc	gss	tac	cgc	tgc	cac	tgc	2688	
W-->	269	His	Gly	Ala	Ser	Cys	Gln	Asn	Thr	His	Gly	Xaa	Tyr	Arg	Cys	His	Cys	
270																	895	
272	cag	gcc	ggc	tac	agt	ggg	cgc	aac	tgc	gag	acc	gac	atc	gac	gac	tgc	2736	
273	Gln	Ala	Gly	Tyr	Ser	Gly	Arg	Asn	Cys	Glu	Thr	Asp	Ile	Asp	Asp	Cys		
274																		
276	cgg	ccc	aac	ccg	tgt	cac	aac	ggg	ggc	tcc	tgc	aca	gac	ggc	atc	aac	2784	
277	Arg	Pro	Asn	Pro	Cys	His	Asn	Gly	Gly	Ser	Cys	Thr	Asp	Gly	Ile	Asn		
278																		
280	acg	gcc	ttc	tgc	gac	tgc	ctg	ccc	ggc	ttc	cgg	ggc	act	ttc	tgt	gag	2832	
281	Thr	Ala	Phe	Cys	Asp	Cys	Leu	Pro	Gly	Phe	Arg	Gly	Thr	Phe	Cys	Glu		
282																		
284	gag	gac	atc	aac	gag	tgt	gcc	agt	gac	ccc	tgc	cgc	aac	ggg	gcc	aac	2880	
285	Glu	Asp	Ile	Asn	Glu	Cys	Ala	Ser	Asp	Pro	Cys	Arg	Asn	Gly	Ala	Asn		
286																		
288	tgc	acg	gac	tgc	gtg	gac	agc	tac	acg	tgc	acc	ttc	ccc	gca	ggc	ttc	2928	
289	Cys	Thr	Asp	Cys	Val	Asp	Ser	Tyr	Thr	Cys	Thr	Cys	Pro	Ala	Gly	Phe		
290																		
292	agc	ggg	atc	cac	tgt	gag	aac	aac	acg	cct	gac	tgc	aca	gag	agc	tcc	2976	
293	Ser	Gly	Ile	His	Cys	Glu	Asn	Asn	Thr	Pro	Asp	Cys	Thr	Glu	Ser	Ser		
294																		
296	tgc	ttc	aac	ggt	ggc	acc	tgc	gtg	gac	ggc	atc	aac	tcg	ttc	acc	tgc	3024	
297	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Val	Asp	Gly	Ile	Asn	Ser	Phe	Thr	Cys		
298																		
300	ctg	tgt	cca	ccc	ggc	ttc	acg	ggc	agc	tac	tgc	cag	cac	gta	gtc	3069		
301	Leu	Cys	Pro	Pro	Gly	Phe	Thr	Gly	Ser	Tyr	Cys	Gln	His	Val	Val			
302																		
304	aat	gag	tgc	gac	tca	cga	ccc	tgc	ctg	cta	ggc	ggc	acc	tgt	cag	3114		
305	Asn	Glu	Cys	Asp	Ser	Arg	Pro	Cys	Leu	Leu	Gly	Gly	Thr	Cys	Gln			
306																		
308	gac	ggt	cgc	ggt	ctc	cac	agg	tgc	acc	tgc	ccc	cag	ggc	tac	act	3159		
309	Asp	Gly	Arg	Gly	Leu	His	Arg	Cys	Thr	Cys	Pro	Gln	Gly	Tyr	Thr			
310																		
312	ggc	ccc	aac	tgc	cag	aac	ctt	gtg	cac	tgg	tgt	gac	tcc	tgc	ccc	3204		
313	Gly	Pro	Asn	Cys	Gln	Asn	Leu	Val	His	Trp	Cys	Asp	Ser	Ser	Pro			
314																		
316	tgc	aag	aac	ggc	ggc	aaa	tgc	tgg	cag	acc	cac	acc	cag	tac	cgc	3249		
317	Cys	Lys	Asn	Gly	Gly	Lys	Cys	Trp	Gln	Thr	His	Thr	Gln	Tyr	Arg			
318																		
320	tgc	gag	tgc	ccc	agc	ggc	tgg	acc	ggc	ctt	tac	tgc	gac	gtg	ccc	3294		
321	Cys	Glu	Cys	Pro	Ser	Gly	Trp	Thr	Gly	Leu	Tyr	Cys	Asp	Val	Pro			
322																		
324	agc	gtg	tcc	tgt	gag	gtg	gct	gcg	cag	cga	caa	ggt	gtt	gac	gtt	3339		
325	Ser	Val	Ser	Cys	Glu	Val	Ala	Ala	Gln	Arg	Gln	Gly	Val	Asp	Val			
326																		
328	gcc	cgc	ctg	tgc	cag	cat	gga	ggg	ctc	tgt	gtg	gac	gcg	ggc	aac	3384		
329	Ala	Arg	Leu	Cys	Gln	His	Gly	Gly	Leu	Cys	Val	Asp	Ala	Gly	Asn			
330																		

→ Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/944,849

DATE: 09/21/2001
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Input Set : A:\ES.txt
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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:500 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:2598 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:2618 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:2638 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
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